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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁷ : C12Q 1/68	A2	(11) International Publication Number: WO 00/55364 (43) International Publication Date: 21 September 2000 (21.09.00)
(21) International Application Number: PCT/GB00/00916 (22) International Filing Date: 10 March 2000 (10.03.00) (30) Priority Data: 99301933.0 12 March 1999 (12.03.99) EP (71) Applicant (for all designated States except US): AMERSHAM PHARMACIA BIOTECH UK LIMITED [GB/GB]; Amer-sham Place, Little Chalfont, Buckinghamshire HP7 9NA (GB). (72) Inventors; and (75) Inventors/Applicants (for US only): <u>REEVE</u> , Michael, Alan [GB/GB]; 118 St Andrews Road, Henley-on-Thames, Ox-fordshire RG9 1PL (GB). <u>WORKMAN</u> , Nicholas, Ian [GB/GB]; 4 Canford Court, Aylesbury, Buckinghamshire HP21 7NZ (GB). <u>MARTIN-PARRAS</u> , Luis [ES/GB]; 7 Gladstone Rise, High Wycombe, Buckinghamshire HP13 7NW (GB). (74) Agents: PENNANT, Pyers et al.; Stevens Hewlett & Perkins, Halton House, 20/23 Holborn, London EC1N 2JD (GB).		(81) Designated States: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Published <i>Without international search report and to be republished upon receipt of that report.</i>
(54) Title: GENETIC ANALYSIS (57) Abstract A method is described for use in whole genome analysis. The method – termed inter–population perfectly matched duplex depletion – can overcome many of the limitations of current approaches based upon SNPs and linkage disequilibrium within isolated populations. Inter–population perfectly matched duplex depletion isolates a fragment (or fragments) containing differences between the "affected" and "unaffected" populations or cells. A convenient method – terminal restriction site profiling arrays (TRSPAs) – is described for the analysis of such fragments. A totally diagnostic internal control DNA is also described which allows both the extent and exact nature of any partial digestion to be unambiguously determined for inter–population perfectly matched duplex depletion or TRSPA restriction.		

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